ABSTRACT OF THE DISCLOSURE

In automatically designing a base sequence to be
used as a probe which is hybridized with an unknown
nucleic acid fragment to perform gene analysis, a
5   discrimination tree in which a plurality of partial base
sequences obtained from target base sequence data are
arranged on nodes is generated. The suitability as a
probe of a partial base sequence represented by a
desired node is evaluated. A plurality of partial base
10   sequences are grouped on the basis of specificity, and
an appropriate group combination is selected. A partial
base sequence to be used as a probe is determined, from
partial base sequences belonging to the selected groups,
on the basis of the evaluation result. In this manner, a
15   probe appropriate for analysis can be automatically
selected in accordance with a target base sequence to be
analyzed. This effectively supports probe designing.